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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:40:16 : Search time 12.47 Seconds
(without alignments)
39.701 Million cell updates/sec

Title: US-08-940-096-146

Sequence: 1 PVLELFENLIERLLDALQKRLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 132412

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCITUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB | ID | Description |
|------------|-------|--------------|----|----|-------------------------------------|
| 1 | 105 | 100.0 | 22 | 3 | US-08-940-095-146 Sequence 146, App |
| 2 | 105 | 100.0 | 22 | 3 | US-08-940-095-174 Sequence 146, App |
| 3 | 105 | 100.0 | 22 | 3 | US-08-940-093-146 Sequence 146, App |
| 4 | 105 | 100.0 | 22 | 3 | US-08-940-093-174 Sequence 146, App |
| 5 | 105 | 100.0 | 22 | 3 | US-08-940-096-146 Sequence 146, App |
| 6 | 105 | 100.0 | 22 | 3 | US-08-940-096-174 Sequence 146, App |
| 7 | 105 | 100.0 | 22 | 4 | US-09-465-719-146 Sequence 146, App |
| 8 | 105 | 100.0 | 22 | 4 | US-09-465-719-174 Sequence 146, App |
| 9 | 102 | 97.1 | 22 | 3 | US-08-940-095-150 Sequence 150, App |
| 10 | 102 | 97.1 | 22 | 3 | US-08-940-095-159 Sequence 150, App |
| 11 | 102 | 97.1 | 22 | 3 | US-08-940-095-169 Sequence 159, App |
| 12 | 102 | 97.1 | 22 | 3 | US-08-940-095-179 Sequence 179, App |
| 13 | 102 | 97.1 | 22 | 3 | US-08-940-095-188 Sequence 188, App |
| 14 | 102 | 97.1 | 22 | 3 | US-08-940-093-150 Sequence 150, App |
| 15 | 102 | 97.1 | 22 | 3 | US-08-940-093-159 Sequence 159, App |
| 16 | 102 | 97.1 | 22 | 3 | US-08-940-093-169 Sequence 169, App |
| 17 | 102 | 97.1 | 22 | 3 | US-08-940-093-179 Sequence 179, App |
| 18 | 102 | 97.1 | 22 | 3 | US-08-940-093-188 Sequence 188, App |
| 19 | 102 | 97.1 | 22 | 3 | US-08-940-096-150 Sequence 150, App |
| 20 | 102 | 97.1 | 22 | 3 | US-08-940-096-159 Sequence 159, App |
| 21 | 102 | 97.1 | 22 | 3 | US-08-940-096-169 Sequence 169, App |
| 22 | 102 | 97.1 | 22 | 3 | US-08-940-096-179 Sequence 179, App |
| 23 | 102 | 97.1 | 22 | 3 | US-08-940-096-188 Sequence 188, App |
| 24 | 102 | 97.1 | 22 | 4 | US-09-465-719-150 Sequence 150, App |
| 25 | 102 | 97.1 | 22 | 4 | US-09-465-719-159 Sequence 159, App |
| 26 | 102 | 97.1 | 22 | 4 | US-09-465-719-169 Sequence 169, App |
| 27 | 102 | 97.1 | 22 | 4 | US-09-465-719-179 Sequence 179, App |

| | | | | | |
|----|-----|------|----|---|-------------------------------------|
| 28 | 102 | 97.1 | 22 | 4 | US-09-465-719-188 Sequence 188, App |
| 29 | 101 | 96.2 | 22 | 3 | US-08-940-095-147 Sequence 147, App |
| 30 | 101 | 96.2 | 22 | 3 | US-08-940-095-152 Sequence 152, App |
| 31 | 101 | 96.2 | 22 | 3 | US-08-940-095-157 Sequence 157, App |
| 32 | 101 | 96.2 | 22 | 3 | US-08-940-095-161 Sequence 161, App |
| 33 | 101 | 96.2 | 22 | 3 | US-08-940-093-147 Sequence 147, App |
| 34 | 101 | 96.2 | 22 | 3 | US-08-940-093-152 Sequence 152, App |
| 35 | 101 | 96.2 | 22 | 3 | US-08-940-093-157 Sequence 157, App |
| 36 | 101 | 96.2 | 22 | 3 | US-08-940-096-147 Sequence 147, App |
| 37 | 101 | 96.2 | 22 | 3 | US-08-940-096-152 Sequence 152, App |
| 38 | 101 | 96.2 | 22 | 3 | US-08-940-096-157 Sequence 157, App |
| 39 | 101 | 96.2 | 22 | 3 | US-08-940-096-161 Sequence 161, App |
| 40 | 101 | 96.2 | 22 | 4 | US-09-465-719-147 Sequence 147, App |
| 41 | 101 | 96.2 | 22 | 4 | US-09-465-719-152 Sequence 152, App |
| 42 | 101 | 96.2 | 22 | 4 | US-09-465-719-157 Sequence 157, App |
| 43 | 101 | 96.2 | 22 | 4 | US-09-465-719-161 Sequence 161, App |
| 44 | 101 | 96.2 | 22 | 3 | US-08-940-095-165 Sequence 165, App |
| 45 | 100 | 95.2 | 22 | 3 | US-08-940-095-165 Sequence 165, App |

ALIGNMENTS

RESULT 1
US-08-940-095-146
Sequence 146, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunter
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-4935
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-146

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKLLK 22
Db 1 PVLLEFENLERLLDALOKKLLK 22

RESULT 2

US-08-940-095-174

; Sequence 174 Application US/08940095
; Patent No. 6004925

GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Butner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/940.095

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cornuzzi, Laura A

; REGISTRATION NUMBER: 30,742

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 174:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6004925e

; FEATURE:

; NAME/KEY: Other

; LOCATION: 1...22

; OTHER INFORMATION: All amino acids are in the D-configuration

US-08-940-095-174

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKLLK 22
Db 1 PVLLEFENLERLLDALOKKLLK 22

RESULT 3

US-08-940-093-146

; Sequence 146, Application US/08940093
; Patent No. 6037323

GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Butner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/940.093

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cornuzzi, Laura A

; REGISTRATION NUMBER: 30,742

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 146:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6037323e

US-08-940-093-146

Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLLEFENLERLLDALOKKLLK 22
Db 1 PVLLEFENLERLLDALOKKLLK 22

RESULT 4

US-08-940-093-174

; Sequence 174 Application US/08940093
; Patent No. 6037323

GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Butner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; NUMBER OF SEQUENCES: 258

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA: US/08/940.093
APPLICATION NUMBER: 009196-0006-999
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
FEATURE:
NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-08-940-093-174
Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
1 PYLELFENLERLLDALOKK 22
1 PYLELFENLERLLDALOKK 22
DB
- RESULT 5
US-08-940-096-146
Sequence 146, Application US/08940096
GENERAL INFORMATION:
PATENT No. 6046166
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornu, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: APOLOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA: US/08/940.096
APPLICATION NUMBER: 009196-0005-999
FILING DATE: 29-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6046166e
US-08-940-096-146
Query Match 100.0%; Score 105; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e-08; 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;
1 PYLELFENLERLLDALOKK 22
1 PYLELFENLERLLDALOKK 22
DB
- RESULT 6
US-08-940-096-174
Sequence 174, Application US/08940096
GENERAL INFORMATION:
PATENT No. 6046166
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornu, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: APOLOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA: US/08/940.096
APPLICATION NUMBER: 009196-0005-999
FILING DATE: 29-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:

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TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: No. 6046166
NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-08-940-096-174

Query Match
Best Local Similarity 100.0%; Score 105; DB 3; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

RESULT 7
US-09-465-719-146
Sequence 146 Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cotruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: No. 6265377e

US-09-465-719-146

Query Match
Best Local Similarity 100.0%; Score 105; DB 4; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

RESULT 8
US-09-465-719-174
Sequence 174 Application US/09465719
Patent No. 6265377
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cotruzzi, Laura A
REGISTRATION NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
FEATURE: No. 6265377e
NAME/KEY: Other
LOCATION: 1...22
OTHER INFORMATION: All amino acids are in the D-configuration
US-09-465-719-174

Query Match
Best Local Similarity 100.0%; Score 105; DB 4; Length 22;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVELEFENLERLDAOKK 22
DB 1 PVELEFENLERLDAOKK 22

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RESULT 9
US-08-940-095-150
Sequence 150, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-150

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0;

OY 1 PVLLEFENLERLDALOKKIK 22
DB 1 PVLLEFENLERLDALOKKIK 22

RESULT 10
US-08-940-095-159
Sequence 159, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6004925e
US-08-940-095-159

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08; Indels 0; Gaps 0;
Matches 21; Conservative 1; Mismatches 0;

OY 1 PVLLEFENLERLDALOKKIK 22
DB 1 PVLLEFENLERLDALOKKIK 22

RESULT 11
US-08-940-095-169
Sequence 169, Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-169

Query Match
Best Local Similarity 97.1%; Score 102; DB 3; Length 22;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVLELFENLERLDAOKK 22
Db 1 PVLELFENLERLDAOKK 22

RESULT 12
US-08-940-095-179
Sequence 179; Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-179

Query Match
Best Local Similarity 97.1%; Score 102; DB 3; Length 22;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PVLELFENLERLDAOKK 22
Db 1 PVLELFENLERLDAOKK 22

RESULT 13
US-08-940-095-188
Sequence 188; Application US/08940095
Patent No. 6004925
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESSES:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6004925e
US-08-940-095-188

Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLLEFENLERLDLOKRLK 22
1 PVLLEFENLERLDLOKRLK 22
DB 1 PVLLEFENLERLDLOKRLK 22

RESULT 14
US-08-940-093-150
Sequence 150, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-150
Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940.093
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6037323e
US-08-940-093-150
Query Match 97.1%; Score 102; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 5.2e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: November 20, 2001, 09:43:25
Job time: 189 sec

Tue Nov 20 10:24:50 2001

us-08-940-096-146.nov20.ra1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:39:15 : Search time 17.78 Seconds
(without alignments)
75.013 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 1 PVLLEFENLEIRLDALQKLLK 22
Sequence:

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 187964

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq.0601:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
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12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
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14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 105 | 100.0 | 22 | AAV19107 | Lecithin:cholester |
| 2 | 105 | 100.0 | 22 | AAV19079 | Lecithin:cholester |
| 3 | 105 | 100.0 | 22 | AAV18853 | Lecithin:cholester |
| 4 | 105 | 100.0 | 22 | AAV18825 | Lecithin:cholester |
| 5 | 105 | 100.0 | 22 | AAV18590 | Lecithin:cholester |
| 6 | 105 | 100.0 | 22 | AAV18562 | Lecithin:cholester |
| 7 | 105 | 100.0 | 22 | AAV19361 | Lecithin:cholester |
| 8 | 105 | 100.0 | 22 | AAV19333 | Lecithin:cholester |
| 9 | 102 | 97.1 | 22 | AAV19375 | Lecithin:cholester |
| 10 | 102 | 97.1 | 22 | AAV19346 | Lecithin:cholester |
| 11 | 102 | 97.1 | 22 | AAV19356 | Lecithin:cholester |

| | | | | | |
|----|-----|------|----|----------|--------------------|
| 12 | 102 | 97.1 | 22 | AAV19112 | Lecithin:cholester |
| 13 | 102 | 97.1 | 22 | AAV19121 | Lecithin:cholester |
| 14 | 102 | 97.1 | 22 | AAV19102 | Lecithin:cholester |
| 15 | 102 | 97.1 | 22 | AAV19083 | Lecithin:cholester |
| 16 | 102 | 97.1 | 22 | AAV19092 | Lecithin:cholester |
| 17 | 102 | 97.1 | 22 | AAV18858 | Lecithin:cholester |
| 18 | 102 | 97.1 | 22 | AAV18867 | Lecithin:cholester |
| 19 | 102 | 97.1 | 22 | AAV18848 | Lecithin:cholester |
| 20 | 102 | 97.1 | 22 | AAV18829 | Lecithin:cholester |
| 21 | 102 | 97.1 | 22 | AAV18838 | Lecithin:cholester |
| 22 | 102 | 97.1 | 22 | AAV18595 | Lecithin:cholester |
| 23 | 102 | 97.1 | 22 | AAV18604 | Lecithin:cholester |
| 24 | 102 | 97.1 | 22 | AAV18575 | Lecithin:cholester |
| 25 | 102 | 97.1 | 22 | AAV18585 | Lecithin:cholester |
| 26 | 102 | 97.1 | 22 | AAV18566 | Lecithin:cholester |
| 27 | 102 | 97.1 | 22 | AAV19366 | Lecithin:cholester |
| 28 | 102 | 97.1 | 22 | AAV19337 | Lecithin:cholester |
| 29 | 101 | 96.2 | 22 | AAV19344 | Lecithin:cholester |
| 30 | 101 | 96.2 | 22 | AAV19348 | Lecithin:cholester |
| 31 | 101 | 96.2 | 22 | AAV19080 | Lecithin:cholester |
| 32 | 101 | 96.2 | 22 | AAV19085 | Lecithin:cholester |
| 33 | 101 | 96.2 | 22 | AAV19090 | Lecithin:cholester |
| 34 | 101 | 96.2 | 22 | AAV19094 | Lecithin:cholester |
| 35 | 101 | 96.2 | 22 | AAV18826 | Lecithin:cholester |
| 36 | 101 | 96.2 | 22 | AAV18831 | Lecithin:cholester |
| 37 | 101 | 96.2 | 22 | AAV18836 | Lecithin:cholester |
| 38 | 101 | 96.2 | 22 | AAV18840 | Lecithin:cholester |
| 39 | 101 | 96.2 | 22 | AAV18577 | Lecithin:cholester |
| 40 | 101 | 96.2 | 22 | AAV18563 | Lecithin:cholester |
| 41 | 101 | 96.2 | 22 | AAV18568 | Lecithin:cholester |
| 42 | 101 | 96.2 | 22 | AAV18573 | Lecithin:cholester |
| 43 | 101 | 96.2 | 22 | AAV19334 | Lecithin:cholester |
| 44 | 101 | 96.2 | 22 | AAV19339 | Lecithin:cholester |
| 45 | 100 | 95.2 | 22 | AAV19352 | Lecithin:cholester |

ALIGNMENTS

| RESULT | ID | AAV19107 | standard; Peptide; 22 AA. |
|--------|----|--|---------------------------|
| XX | AC | AAV19107; | |
| XX | DT | 09-JUL-1999 (first entry) | |
| XX | DE | Lecithin:cholesterol acyltransferase activation exhibiting peptide #174. | |
| XX | XX | Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia; | |
| KW | KW | human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia; | |
| KW | KW | cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I; | |
| KW | KW | high density lipoprotein; hypertriglyceridemia; metabolic syndrome; | |
| KW | KW | septic shock. | |
| XX | OS | Synthetic. | |
| OS | OS | Homo sapiens. | |
| XX | FN | W09916458-A1. | |
| XX | PD | 08-APR-1999. | |
| XX | PF | 28-SEP-1998; 98WO-US20326. | |
| XX | PR | 29-SEP-1997; 97US-0940096. | |
| XX | PA | (BUTN) BUTTNER K. | |
| XX | PA | (CORN) CORNU I. | |
| XX | PA | (DASS) DASSEUX J. | |
| XX | PA | (METZ) METZ G. | |
| XX | PA | (SEKU) SEKUL R. | |
| PI | PI | Buttner K, Cornut I, Dasseux J, Metz G, Sekul R; | |

XX DR WPI, 1999-277034/23.

XX PT Peptide agonists of apolipoprotein A-I

XX PS Example; Page 116; 254pp; English.

XX CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoa-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoa-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
 CC AAY19187 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoa-I agonists.

XX SQ Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKIK 22
 DB 1 PVLELFENLERLIDALQKKIK 22

RESULT 2

AAY19079

ID AAY19079 standard; Peptide: 22 AA.

AC AAY19079;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

KW Apolipoprotein A-I; agonist: dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoa-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX OS Synthetic.

OS Homo sapiens.

XX WO916458-A1.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20326.

PR 29-SEP-1997; 97US-0940096.

PA (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (METZ/) METZ G.

PA (SEKU/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

DR WPI, 1999-277034/23.

XX PT Peptide agonists of apolipoprotein A-I

XX PS Claim 18; Page 115; 254pp; English.

XX CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoa-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoa-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
 CC AAY19187 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoa-I agonists.

XX SQ Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLIDALQKKIK 22
 DB 1 PVLELFENLERLIDALQKKIK 22

RESULT 3

AAY18853

ID AAY18853 standard; Peptide: 22 AA.

AC AAY18853;

DT 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

KW Apolipoprotein A-I; agonist: dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoa-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX OS Synthetic.

OS Homo sapiens.

XX WO916408-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20328.

PR 29-SEP-1997; 97US-0940093.

PA (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (METZ/) METZ G.

PA (SEKU/) SEKUL R.

PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;

DR WPI, 1999-277031/23.

XX PT Peptide agonists of apolipoprotein A-I

XX PS Example; Page 113; 152pp; English.

XX CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoa-I) which is a 14-22 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular

CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to
 CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLLEFENLERLDALOKKLK 22
 |||||
 Db 1 pvllefenlerlaldalqkkik 22

RESULT 4

AAY18825 standard; Peptide: 22 AA.

XX AAY18825;
 XX 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX Synthetic.
 OS Homo sapiens.

XX WO9916408-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20328.

XX 29-SEP-1997; 97US-0940093.

XX (BUTT/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.
 PA (METZ/) METZ G.
 PA (SEKU/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;

XX WPI; 1999-277031/23.

XX Peptide agonists of apolipoprotein A-I

XX Example; Page 112; 152pp; English.

CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 14-22 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18680 to

CC AAY18933 represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLLEFENLERLDALOKKLK 22
 |||||
 Db 1 pvllefenlerlaldalqkkik 22

RESULT 5

AAY18590 standard; Peptide: 22 AA.

XX AAY18590;

XX 09-JUL-1999 (first entry)

DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW ApoA-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

XX Synthetic.
 OS Homo sapiens.

XX WO9916409-A2.

XX 08-APR-1999.

XX 28-SEP-1998; 98WO-US20329.

XX 29-SEP-1997; 97US-0940136.

XX (BUTT/) BUTTNER K.
 PA (CORN/) CORNUT I.
 PA (DASS/) DASSEUX J.
 PA (DUFO/) DUFOURCQ J.
 PA (METZ/) METZ G.
 PA (SEKU/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
 PI Sekul R;

XX WPI; 1999-254921/21.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

XX Example; Page 178; 232pp; English.

CC The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoA-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular disease,
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoA-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also to treat
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoA-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents a peptide from the present invention.

XX Sequence 22 AA:

Query Match 100.0%; Score 105; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLDAQKKLK 22
 Db 1 pvllelfenlerlldaqlqkik 22

RESULT 6
 AAY18562

ID AAY18562 standard; Peptide; 22 AA.

AC AAY18562;

DT 09-JUL-1999 (first entry)

XX Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.

XX Gene therapy; apolipoprotein A-I; agonist; dyslipidemic disorder;
 KW Apoa-I; cardiovascular disease; atherosclerosis; restenosis; LCAT;
 KW hyperlipidemia; septic shock; lecithin:cholesterol acyltransferase.

XX Synthetic.

OS Homo sapiens.

XX WO9916409-A2.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20329.

PR 29-SEP-1997; 97US-0940136.

XX (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DUFO/) DUFOURCO J.

PA (METZ/) METZ G.

PA (SEKUL/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

DR WPI: 1999-254921/21.

XX Nucleic acid encoding apolipoprotein A-I agonist peptides

PS Claim 35; Page 170; 232pp; English.

XX The present invention describes a nucleic acid (A) encoding an
 CC apolipoprotein A-I (apoa-I) agonist (B) that is a peptide, or analog,
 CC which forms an amphipathic alpha-helix in presence of lipids. (A),
 CC optionally as a complex with lipids, and host cells that contain (A),
 CC are useful for gene therapy, or prevention, of diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
 CC atherosclerosis, restenosis, HDL (high density lipoprotein) and apoa-I
 CC deficiency, hypertriglyceridemia and metabolic syndrome, also for
 CC endotoxemia (septic shock). Host cells containing (A) can also be used
 CC to study the role of apoa-I in lipid metabolism. (B) can be used
 CC diagnostically, e.g. to measure serum HDL (particularly its
 CC subpopulation involved in retrograde cholesterol transport) and for
 CC imaging the circulatory system or HDL accumulations at fatty streaks.
 CC The present sequence represents a peptide from the present invention.

XX Sequence 22 AA;

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLDAQKKLK 22
 Db 1 pvllelfenlerlldaqlqkik 22

RESULT 7
 AAY19361

ID AAY19361 standard; Peptide; 22 AA.

AC AAY19361;

DT 14-JUL-1999 (first entry)

XX Lecithin:cholesterol acyltransferase activation exhibiting peptide #174.

XX Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoa-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.

XX Synthetic.

OS Homo sapiens.

XX WO9916459-A1.

PD 08-APR-1999.

PF 28-SEP-1998; 98WO-US20327.

PR 29-SEP-1997; 97US-0940095.

XX (BUTT/) BUTTNER K.

PA (CORN/) CORNUT I.

PA (DASS/) DASSEUX J.

PA (DUFO/) DUFOURCO J.

PA (METZ/) METZ G.

PA (SEKUL/) SEKUL R.

PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;

PI Sekul R;

DR WPI: 1999-277035/23.

XX Peptide agonists of apolipoprotein A-I

PS Example; Page 125; 280pp; English.

XX The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoa-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoa-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
 CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoa-I agonists.

XX Sequence 22 AA;

Query Match 100.0%; Score 105; DB 20; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.3e-08;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PVLELFENLERLDAQKKLK 22
 Db 1 pvllelfenlerlldaqlqkik 22

```

RESULT      8
AAV19333
ID AAV19333 standard; Peptide: 22 AA.
XX
AC AAV19333;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #146.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO916459-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US20327.
XX
PR 29-SEP-1997; 97US-0940095.
XX
PA (BUTTNER K. BUTTNER K.
PA (CORNUT I. CORNUT I.
PA (DASSEUX J. DASSEUX J.
PA (DUFOURCQ J. DUFOURCQ J.
PA (METZ G. METZ G.
PA (SEKUL R. SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
PI Sekul R;
XX
DR WPI: 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I
XX
PS Example: Page 124; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAV19188 to
CC AAV19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.
XX
SQ Sequence 22 AA:

```

```

Query Match 100.0%; Score 105; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2, 3e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 PVLLEFENLERLDAIÖKKLK 22
   |||
DB 1 pvllefenlerlidaikkkik 22

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RESULT      9
AAV19375
ID AAV19375 standard; Peptide: 22 AA.

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XX
AC AAV19375;
XX
DT 14-JUL-1999 (first entry)
XX
DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #188.
XX
KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
KW septic shock.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO916459-A1.
XX
PD 08-APR-1999.
XX
PF 28-SEP-1998; 98WO-US20327.
XX
PR 29-SEP-1997; 97US-0940095.
XX
PA (BUTTNER K. BUTTNER K.
PA (CORNUT I. CORNUT I.
PA (DASSEUX J. DASSEUX J.
PA (DUFOURCQ J. DUFOURCQ J.
PA (METZ G. METZ G.
PA (SEKUL R. SEKUL R.
XX
PI Buttner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
PI Sekul R;
XX
DR WPI: 1999-277035/23.
XX
PT Peptide agonists of apolipoprotein A-I
XX
PS Example: Page 126; 280pp; English.
XX
CC The present invention describes an agonist (A) of apolipoprotein A-I
CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
CC complexes, are used to treat or prevent diseases associated with
CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
CC treating septic shock. When labeled, (A) can also be used diagnostically
CC to measure serum levels of HDL, in particular the HDL subpopulation that
CC is involved in retrograde cholesterol transport, also to image HDL at
CC e.g. atherosclerotic streaks, and to raise antibodies. AAV19188 to
CC AAV19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
CC exhibiting core peptides, which are apoA-I agonists.
XX
SQ Sequence 22 AA:

```

```

Query Match 97.1%; Score 102; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 6e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PVLLEFENLERLDAIÖKKLK 22
   |||
DB 1 pvllefenlerlidaikkkik 22

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RESULT      10
AAV19346
ID AAV19346 standard; Peptide: 22 AA.

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XX
AC AAV19346;
XX
DT 14-JUL-1999 (first entry)

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XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #159.
XX DE Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
XX KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
XX KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
XX KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
XX KW septic shock.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN MO9916459-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US20327.
XX PR 29-SEP-1997; 97US-0940095.
XX PA (BUTT/) BUTTNER K.
XX PA (CORN/) CORNUT I.
XX PA (DASS/) DASSEUX J.
XX PA (DUFO/) DUFOURCQ J.
XX PA (METZ/) METZ G.
XX PA (SEKU/) SEKUL R.
XX PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
XX PI Sekul R;
XX DR WPI: 1999-277035/23.
XX PS Peptide agonists of apolipoprotein A-I
XX PT Example: Page 124; 280pp; English.
XX XX
XX CC The present invention describes an agonist (A) of apolipoprotein A-I
XX CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
XX CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
XX CC complexes, are used to treat or prevent diseases associated with
XX CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
XX CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
XX CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
XX CC treating septic shock. When labeled, (A) can also be used diagnostically
XX CC to measure serum levels of HDL. In particular the HDL subpopulation that
XX CC is involved in retrograde cholesterol transport, also to image HDL at
XX CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
XX CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
XX CC exhibiting core peptides, which are apoA-I agonists.
XX SO Sequence 22 AA:

```

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvlidfenllrlldalqkrlk 22

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RESULT 11
AAY19356
ID AAY19356 standard; Peptide; 22 AA.
AC AAY19356;
XX
XX 14-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #169.
XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
XX KW septic shock.

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KW KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
KW KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
KW KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
XX KW septic shock.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN MO9916459-A1.
XX PD 08-APR-1999.
XX PF 28-SEP-1998; 98WO-US20327.
XX PR 29-SEP-1997; 97US-0940095.
XX PA (BUTT/) BUTTNER K.
XX PA (CORN/) CORNUT I.
XX PA (DASS/) DASSEUX J.
XX PA (DUFO/) DUFORCQ J.
XX PA (METZ/) METZ G.
XX PA (SEKU/) SEKUL R.
XX PI Butner K, Cornut I, Dasseux J, Dufourcq J, Metz G;
XX PI Sekul R;
XX DR WPI: 1999-277035/23.
XX PS Peptide agonists of apolipoprotein A-I
XX PT Example: Page 125; 280pp; English.
XX XX
XX CC The present invention describes an agonist (A) of apolipoprotein A-I
XX CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
XX CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
XX CC complexes, are used to treat or prevent diseases associated with
XX CC dyslipidemia, specifically hypercholesterolemia, cardiovascular
XX CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
XX CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
XX CC treating septic shock. When labeled, (A) can also be used diagnostically
XX CC to measure serum levels of HDL. In particular the HDL subpopulation that
XX CC is involved in retrograde cholesterol transport, also to image HDL at
XX CC e.g. atherosclerotic streaks, and to raise antibodies. AAY19188 to
XX CC AAY19441 represent lecithin:cholesterol acyltransferase (LCAT) activity
XX CC exhibiting core peptides, which are apoA-I agonists.
XX SO Sequence 22 AA:

```

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvlidfenllrlldalqkrlk 22

```

RESULT 12
AAY19112
ID AAY19112 standard; Peptide; 22 AA.
AC AAY19112;
XX
XX 09-JUL-1999 (first entry)
XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #179.
XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
XX KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolemia;
XX KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
XX KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
XX KW septic shock.

```

XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN MO9916458-A1.
 XX PD 08-APR-1999.
 XX PF 28-SEP-1998; 98MO-US20326.
 XX PR 29-SEP-1997; 97US-0940096.
 XX PA (BUTT/) BUTTNER K.
 XX PA (CORN/) CORNUT I.
 XX PA (DASS/) DASSEUX J.
 XX PA (METZ/) METZ G.
 XX PA (SEKU/) SEKUL R.
 XX PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;
 XX PS WPI: 1999-277034/23.
 XX DR Peptide agonists of apolipoprotein A-I
 XX PT Example: Page 116; 254pp; English.
 XX PS The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAV18934 to AAV19187 represent lecitin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:
 Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvllelfenlrlldalqkrlk 22

RESULT 13
 AAV19121
 ID AAV19121 standard; Peptide: 22 AA.
 AC AAV19121;
 XX 09-JUL-1999 (first entry)
 XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #188.
 XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN MO9916458-A1.

PD 08-APR-1999.
 XX PF 28-SEP-1998; 98MO-US20326.
 XX PR 29-SEP-1997; 97US-0940096.
 XX PA (BUTT/) BUTTNER K.
 XX PA (CORN/) CORNUT I.
 XX PA (DASS/) DASSEUX J.
 XX PA (METZ/) METZ G.
 XX PA (SEKU/) SEKUL R.
 XX PI Butner K, Cornut I, Dasseux J, Metz G, Sekul R;
 XX PS WPI: 1999-277034/23.
 XX DR Peptide agonists of apolipoprotein A-I
 XX PT Claim 18; Page 117; 254pp; English.
 XX PS The present invention describes an agonist (A) of apolipoprotein A-I (apoA-I) which is a 15-29 residue peptide, or analog, that forms an amphipathic alpha-helix in presence of lipids. (A), and their lipid complexes, are used to treat or prevent diseases associated with dyslipidemia, specifically hypercholesterolaemia, cardiovascular disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for treating septic shock. When labeled, (A) can also be used diagnostically to measure serum levels of HDL, in particular the HDL subpopulation that is involved in retrograde cholesterol transport, also to image HDL at e.g. atherosclerotic streaks, and to raise antibodies. AAV18934 to AAV19187 represent lecitin:cholesterol acyltransferase (LCAT) activity exhibiting core peptides, which are apoA-I agonists.

SO Sequence 22 AA:
 Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PVLELFENLRLDALQKRLK 22
 DB 1 pvllelfenlrlldalqkrlk 22

RESULT 14
 AAV19102
 ID AAV19102 standard; Peptide: 22 AA.
 AC AAV19102;
 XX 09-JUL-1999 (first entry)
 XX DE Lecithin:cholesterol acyltransferase activation exhibiting peptide #189.
 XX KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN MO9916458-A1.
 XX PD 08-APR-1999.
 XX PF 28-SEP-1998; 98MO-US20326.
 XX PR 29-SEP-1997; 97US-0940096.

PA (BUTTNER K.
 PA (CORNUT I.
 PA (DASSEUX J.
 PA (METZ G.
 PA (SEKUL R.
 XX
 PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
 DR WPI: 1999-277034/23.
 XX
 PT Peptide agonists of apolipoprotein A-I
 PS
 XX Example: Page 116; 254pp; English.
 XX The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
 CC AAY19187 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.
 XX
 SQ Sequence 22 AA:

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08; 0; Indels 0; Gaps 0;
 Matches 21; Conservative 1; Mismatches 0;
 QY 1 PVLLEFENLIERLDAOKK 22
 Db 1 PVLLEFENLIERLDAOKK 22

RESULT 15
 AAY19083
 ID AAY19083 standard; Peptide: 22 AA.
 XX
 AC AAY19083;
 XX
 DT 09-JUL-1999 (first entry)
 XX
 DE
 XX
 XX Lecithin:cholesterol acyltransferase activation exhibiting peptide #150.
 KW Apolipoprotein A-I; agonist; dyslipidemic disorder; dyslipidemia;
 KW human; lecithin:cholesterol acyltransferase; LCAT; hypercholesterolaemia;
 KW cardiovascular disease; atherosclerosis; restenosis; HDL; apoA-I;
 KW high density lipoprotein; hypertriglyceridemia; metabolic syndrome;
 KW septic shock.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN M09916458-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 28-SEP-1998; 98WO-US20326.
 XX
 PR 29-SEP-1997; 97US-0940096.
 XX
 PA (BUTTNER K.
 PA (CORNUT I.
 PA (DASSEUX J.
 PA (METZ G.
 PA (SEKUL R.
 XX

PI Buttner K, Cornut I, Dasseux J, Metz G, Sekul R;
 DR WPI: 1999-277034/23.
 XX
 PT Peptide agonists of apolipoprotein A-I
 PS
 XX Claim 18; Page 115; 254pp; English.
 XX

CC The present invention describes an agonist (A) of apolipoprotein A-I
 CC (apoA-I) which is a 15-29 residue peptide, or analog, that forms an
 CC amphipathic alpha-helix in presence of lipids. (A), and their lipid
 CC complexes, are used to treat or prevent diseases associated with
 CC dyslipidemia, specifically hypercholesterolaemia, cardiovascular
 CC disease, atherosclerosis, restenosis, HDL (high density lipoprotein) or
 CC apoA-I deficiency; hypertriglyceridemia and metabolic syndrome, also for
 CC treating septic shock. When labeled, (A) can also be used diagnostically
 CC to measure serum levels of HDL, in particular the HDL subpopulation that
 CC is involved in retrograde cholesterol transport, also to image HDL at
 CC e.g. atherosclerotic streaks, and to raise antibodies. AAY18934 to
 CC AAY19187 represent lecitin:cholesterol acyltransferase (LCAT) activity
 CC exhibiting core peptides, which are apoA-I agonists.
 XX
 SQ Sequence 22 AA:

Query Match 97.1%; Score 102; DB 20; Length 22;
 Best Local Similarity 95.5%; Pred. No. 6e-08;
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PVLLEFENLIERLDAOKK 22
 Db 1 PVLLEFENLIERLDAOKK 22

Search completed: November 20, 2001, 09:43:06
 Job time: 231 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2001, 09:41:06 ; Search time 12.74 Seconds
(without alignments)
131.542 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 105
Sequence: 1 PYLEFENLERLDALQKKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 6208

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 35 | 33.3 | 26 | 2 | H64589 |
| 2 | 32 | 30.5 | 24 | 2 | H48368 |
| 3 | 31.5 | 30.0 | 29 | 2 | B85840 |
| 4 | 31.5 | 30.0 | 29 | 2 | C85840 |
| 5 | 31 | 29.5 | 21 | 1 | A35225 |
| 6 | 31 | 29.5 | 30 | 1 | OEON2K |
| 7 | 27 | 25.7 | 24 | 2 | T43971 |
| 8 | 27 | 25.7 | 25 | 2 | PC4445 |
| 9 | 27 | 25.7 | 26 | 2 | PL0027 |
| 10 | 26 | 24.8 | 24 | 2 | A20554 |
| 11 | 26 | 24.8 | 24 | 2 | G20554 |
| 12 | 26 | 24.8 | 24 | 2 | H20554 |
| 13 | 26 | 24.8 | 26 | 2 | S62672 |
| 14 | 26 | 24.8 | 26 | 2 | S02788 |
| 15 | 26 | 24.8 | 28 | 2 | A23691 |
| 16 | 26 | 24.8 | 30 | 2 | H70152 |
| 17 | 25 | 23.8 | 26 | 2 | F20554 |
| 18 | 25 | 23.8 | 29 | 2 | S51070 |
| 19 | 25 | 23.8 | 29 | 2 | CS4037 |
| 20 | 25 | 23.8 | 29 | 2 | A49410 |
| 21 | 24 | 22.9 | 14 | 2 | S13864 |
| 22 | 24 | 22.9 | 16 | 2 | S65709 |
| 23 | 24 | 22.9 | 20 | 2 | C20554 |
| 24 | 24 | 22.9 | 23 | 4 | A58505 |
| 25 | 24 | 22.9 | 25 | 2 | D20554 |
| 26 | 24 | 22.9 | 25 | 2 | G41606 |
| 27 | 24 | 22.9 | 26 | 1 | B57082 |
| 28 | 24 | 22.9 | 27 | 1 | SEBO |
| 29 | 24 | 22.9 | 27 | 1 | SESH |

ALIGNMENTS

| | | | | | | |
|----|----|------|----|---|--------|--------------------|
| 30 | 24 | 22.9 | 27 | 2 | A44641 | homeotic protein H |
| 31 | 23 | 21.9 | 14 | 2 | I51430 | hemoglobin beta ch |
| 32 | 23 | 21.9 | 20 | 2 | S63602 | glutathione S-tran |
| 33 | 23 | 21.9 | 22 | 2 | I58038 | MHC class I transp |
| 34 | 23 | 21.9 | 22 | 2 | A37335 | 68k surface antige |
| 35 | 23 | 21.9 | 23 | 2 | A33948 | glutathione transi |
| 36 | 23 | 21.9 | 24 | 2 | A45336 | cystic fibrosis tr |
| 37 | 23 | 21.9 | 24 | 2 | I39680 | exer protein - Aer |
| 38 | 23 | 21.9 | 24 | 2 | B27262 | nicotinic acetylch |
| 39 | 23 | 21.9 | 26 | 2 | A40630 | delta hemolysin - |
| 40 | 23 | 21.9 | 26 | 2 | A40630 | hypothetical prote |
| 41 | 23 | 21.9 | 26 | 2 | F69265 | hypothetical prote |
| 42 | 23 | 21.9 | 26 | 4 | I55277 | hemoglobin alpha c |
| 43 | 23 | 21.9 | 27 | 1 | S07443 | secretin - human |
| 44 | 23 | 21.9 | 27 | 2 | A27267 | secretin - dog |
| 45 | 23 | 21.9 | 27 | 2 | C60415 | secretin - rabbit |

RESULT 1
H64589
hypothetical protein (HP0560, jhp0507) - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variate: strains J99, 26695
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: H64589; A71923
R:Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKee,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: H64589
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <TOM>
A:Cross-references: GB:AE000570; GB:AE000511; NID:g2313672; PIDN:AA00633.1; PID:g231
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Molt, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.
; Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557
A:Accession: A71923
A:Molecule type: DNA
A:Residues: 1-26 <ARN>
A:Cross-references: GB:AE001484; GB:AE001439; NID:g4155043; PIDN:AA006083.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: HP0560; jhp0507

Query Match 33.3%; Score 35; DB 2; Length 26;
Best Local Similarity 58.3%; Pred. No. 97;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LERLDALQKK 20
DB 15 LAYRIIDVLEQK 26

RESULT 2
B48368
N5,N10-methylethyltetrahydromethanopterin cyclohydrolase - Methanosarcina barkeri (Frag
C:Species: Methanosarcina barkeri
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B48368
R:Klein, A.R.; Breitung, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.
Arch. Microbiol. 159, 213-219, 1993
A:Title: N5,N10-methylethyltetrahydromethanopterin cyclohydrolase from the extremely the

from the extremely thermophilic *Methanopyrus kandleri*.
 A:Reference number: A48368; MUID:93243882

A:Contents: Pusaro D
 A:Accession: B48368

A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <KLE>

A:Note: sequence extracted from NCBI backbone (NCBIP:130470)

Query Match 30.5%; Score 32; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 VLEFENLERLIDALQ 16
 | | | | | | | | | | | | | | | | | | | |
 Db 4 VNMGSNVIEEMLDS 18

RESULT 3
 B85840
 hypothetical protein Z3289 [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

A:Accession: B85840

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85840

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: GB:AE005174; NID:912516340; PIDN:AGS7182.1; GSPDB:GN00145; UWGP:232

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z3289

Query Match 30.0%; Score 31.5; DB 2; Length 29;
 Best Local Similarity 58.8%; Pred. No. 3.4e+02;
 Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 2 VLEFENLERLIDALQ 18
 | | | | | | | | | | | | | | | | | | | |
 Db 14 VLELLVALL-RLIDLK 29

RESULT 4

C85840
 hypothetical protein Z3290 [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

A:Accession: C85840

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C85840

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-29 <STO>

A:Cross-references: GB:AE005174; NID:912516341; PIDN:AGS7183.1; GSPDB:GN00145; UWGP:232

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z3290

Query Match 30.0%; Score 31.5; DB 2; Length 29;
 Best Local Similarity 58.8%; Pred. No. 3.4e+02;
 Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 2 VLEFENLERLIDALQ 18
 | | | | | | | | | | | | | | | | | | | |
 Db 14 VLELLVALL-RLIDLK 29

RESULT 5
 A35225
 conantokin T - cone shell (*Conus tulipa*)

N:Alternate names: sleeper peptide

C:Species: *Conus tulipa* (tulip cone)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: A35225

R:Haack, J.A.; Rivier, J.; Parks, T.N.; Mena, E.E.; Cruz, L.J.; Olivera, B.M.

J. Biol. Chem. 265, 6025-6029, 1990

A:Title: Conantokin-T, A gamma-carboxyglutamate containing peptide with N-methyl-D-as

A:Reference number: A35225; MUID:90202866

A:Accession: A35225

A:Molecule type: protein

A:Residues: 1-2, 'XX', 5-9, 'X', 11-13, 'X', 15-21 <HAA>

A:Note: the residues designated 'X' were determined to be gamma-carboxy glutamic acid

C:Comment: This venom peptide induces sleep in young mice and is an NMDA antagonist 1

C:Superfamily: conantokin

C:Keywords: amidated carboxyl end; carboxyglutamic acid; neurotoxin; venom

F:3,4,10,14/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental

F:21/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 29.5%; Score 31; DB 1; Length 21;
 Best Local Similarity 41.2%; Pred. No. 2.8e+02;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 4 ELFENLERLIDALQ 20
 | | | | | | | | | | | | | | | | | | | |
 Db 3 EBYOKMLENLEAEVKK 19

RESULT 6

OEON2K
 beta-endorphin II - chum salmon

N:Contains: Met-enkephalin

C:Species: *Oncorhynchus keta* (chum salmon)

C:Date: 31-May-1980 #sequence_revision 31-May-1980 #text_change 21-Jan-2000

A:Accession: A01469

R:Kawauchi, H.; Tsubokawa, M.; Kanezawa, A.; Kitagawa, H.

Biochem. Biophys. Res. Commun. 92, 1278-1288, 1980

A:Title: Occurrence of two different endorphins in the salmon pituitary.

A:Reference number: A01469; MUID:80174902

A:Accession: A01469

A:Molecule type: protein

A:Residues: 1-30 <KAW>

C:Superfamily: corticotropin-lipotropin

C:Keywords: acetylated amino end; opioid peptide

F:1-5/Product: Met-enkephalin #status predicted <MEN>

F:1/Modified site: acetylated amino end (Tyr) #status experimental

Query Match 29.5%; Score 31; DB 1; Length 30;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PVLEFENL 10
 | | | | | | | | | | | | | | | | | | | |
 Db 15 PLLELFKNVI 24

RESULT 7

T43971
 CC-chemokine receptor [imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6

A:Variety: strain HST

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T43971

| | | | | | |
|-----------------------|-----------------|--------------|--------------|--------|-----|
| Query Match | 25.7%; | Score No. | DB 2; | Length | 26; |
| Best Local Similarity | 35.7%; | Pred | No. 1.3e+03; | | |
| Matches | 5; Conservative | Mismatches | 4; | Indels | 0; |
| Gaps | 0; | | | | |
| QY | 7 | ENTLRLDALOKK | 20 | | |
| I | : | :::: | : | | |
| 9 | EDDKRIIIDDLDAK | 22 | | | |
| db | | | | | |

| | | | | | | | |
|-----------------------|-------|--------------|----------|------------|----|--------|-----|
| Query Match | 24.8% | Score | 26; | DB | 2; | Length | 24; |
| Best Local Similarity | 50.0% | Pred. No. | 1.7e+03; | | | | |
| Matches | 5; | Conservative | 4; | Mismatches | 1; | Indels | 0; |
| | | | | | | Gaps | 0; |

OY 13 LLDALOKKLR 22
 :| | | :
 Db 1 VLGALEKQLR 10

RESULT 13

S62672
 transcobalamin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 02-Jul-1998
 C:Accession: S62672
 R:Redosov, S.N.; Petersen, T.E.; Nexø, E.
 Biochim. Biophys. Acta 1292, 113-119, 1996
 A:Title: Transcobalamin from cow milk: Isolation and physico-chemical properties.
 A:Reference number: S62672; MUID:96139334
 A:Accession: S62672
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-26 <FE0>
 C:Superfamily: gastric intrinsic factor

Query Match 24.8%; Score 26; DB 2; Length 26;
 Best local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 5 LEFNLRLDALOK 19
 | | | : | | :
 Db 12 LVERLGGRLPXMDR 26

RESULT 14

S02788
 arylamine N-acetyltransferase (EC 2.3.1.5) 1 - human (fragments)
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-May-2000
 C:Accession: S02788
 R:Grant, D.M.; Lottspeich, F.; Meyer, U.A.
 FEBS Lett 244, 203-207, 1989
 A:Title: Evidence for two closely related isozymes of arylamine N-acetyltransferase in h
 A:Reference number: S02788; MUID:89171260
 A:Accession: S02788
 A:Molecule type: protein
 A:Residues: 1-17; 18-26 <GRA>
 C:Keywords: acyltransferase; coenzyme A

Query Match 24.8%; Score 26; DB 2; Length 26;
 Best local Similarity 38.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 10 LERLDALOKKLR 22
 | | | | : : : :
 Db 5 LETLDILETQIR 17

RESULT 15

A23691
 apolipoprotein C-I - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 31-Dec-1993
 C:Accession: A23691
 R:Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
 J. Biol. Chem. 265, 22453-22459, 1990
 A:Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migr
 ceptor-related protein.
 A:Reference number: A23691; MUID:91093092
 A:Accession: A23691
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 1-28 <WEI>
 C:Superfamily: apolipoprotein A-I
 C:Keywords: lipid binding; lipoprotein

Query Match 24.8%; Score 26; DB 2; Length 28;
 Best local Similarity 30.0%; Pred. No. 2e+03;
 Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 3 LEFNLRLDALOKKLR 22
 | | | : | : : :
 Db 7 LEIPDKLKEFGNTLEKAR 26

Search completed: November 20, 2001, 09:43:45
 Job time: 159 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2001, 09:43:11 ; Search time 9.9 Seconds
(without alignments)
76.123 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 105
Sequence: 1 PVLELFENLLERLLDALQKKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 1767
```

```
Minimum DB seq length: 0
Maximum DB seq length: 30
```

| | | |
|------------------|---------------|--------------|
| Post-processing: | Minimum Match | 0% |
| | Maximum Match | 100% |
| | Listing first | 45 summaries |

Database : SwissProt_39.*

SUMMARIES

| Result | No. | Score | Query Match | Length | DB | ID | Description |
|--------|-----|-------|-------------|--------|----|------------|---------------------|
| | 1 | 31 | 29.5 | 21 | 1 | CXGT_CONTV | P17684 conus tulip |
| | 2 | 31 | 29.5 | 30 | 1 | END2_OMCKE | P01205 oncorhynch |
| | 3 | 29 | 27.6 | 19 | 1 | NUO6_SOLUT | P80729 solanum tubu |
| | 4 | 28 | 26.7 | 13 | 1 | TEME_RANTE | P56920 rana tempor |
| | 5 | 28 | 26.7 | 27 | 1 | DMS4_PHYSA | P80280 phyllomedus |
| | 6 | 26 | 24.8 | 28 | 1 | APC1_RABIT | P33047 oryctolagus |
| | 7 | 26 | 24.8 | 30 | 1 | V425_BORBU | P51366 borrella bu |
| | 8 | 25 | 23.8 | 10 | 1 | TEMC_RANTE | P65623 rana tempor |
| | 9 | 25 | 23.8 | 23 | 1 | NIFD_ANASL | P33177 anaheena sp |
| | 10 | 25 | 23.8 | 26 | 1 | CT21_LITCI | P81847 litorea cili |
| | 11 | 24 | 22.9 | 13 | 1 | TEMC_RANTE | P56198 rana tempor |
| | 12 | 24 | 22.9 | 13 | 1 | TEMD_RANTE | P56819 rana tempor |
| | 13 | 24 | 22.9 | 27 | 1 | KT39_PICKL | P80326 pichia kluy |
| | 14 | 24 | 22.9 | 27 | 1 | SECR_SHEEP | P31299 ovis aries |
| | 15 | 24 | 22.9 | 28 | 1 | MAAL_RAT | P57113 rattus norv |
| | 16 | 23 | 21.9 | 11 | 1 | UM05_CLOPA | P81350 clostridium |
| | 17 | 23 | 21.9 | 13 | 1 | RPOC_MYCGA | P47716 mycoplasma |
| | 18 | 23 | 21.9 | 23 | 1 | T2A_PARTE | Q27173 parametium |
| | 19 | 23 | 21.9 | 24 | 1 | ACHE_ELEBL | P09689 electrophor |
| | 20 | 23 | 21.9 | 26 | 1 | VGLH_HSVF | P13160 feline herp |
| | 21 | 23 | 21.9 | 27 | 1 | SECR_CANFA | P09910 canis fami |
| | 22 | 23 | 21.9 | 27 | 1 | SECR_RABIT | P32647 oryctolagus |
| | 23 | 23 | 21.9 | 28 | 1 | CH60_MYCSM | P80673 mycobacteri |
| | 24 | 22 | 21.0 | 12 | 1 | FREL_LITIN | P82021 litorea infi |
| | 25 | 22 | 21.0 | 14 | 1 | MAST_VESLE | P01514 vesputia lew |
| | 26 | 22 | 21.0 | 14 | 1 | MAST_VESMA | P04205 vespa manda |
| | 27 | 22 | 21.0 | 15 | 1 | UCZ2_MAIZE | P80633 zea mays (m |
| | 28 | 22 | 21.0 | 17 | 1 | FLA2_BARBA | P35634 bartonella |
| | 29 | 22 | 21.0 | 21 | 1 | BOH5_BOMVA | P82284 bomina var |
| | 30 | 22 | 21.0 | 21 | 1 | BOH5_BOMVA | P82284 bomina var |
| | 31 | 22 | 21.0 | 24 | 1 | CT31_LITCI | P81851 litorea cili |
| | 32 | 22 | 21.0 | 26 | 1 | ACHD_ELEBL | P09691 electrophor |
| | 33 | 22 | 21.0 | 26 | 1 | PUTA_KLEPN | P23725 klebsiella |

| | | | | | |
|----|------|------|----|---|-------------|
| 45 | 21 | 20.0 | 22 | 1 | REV_HY2D2 |
| 44 | 21 | 20.0 | 21 | 1 | UVSX_BP72 |
| 43 | 21 | 20.0 | 20 | 1 | hunan immun |
| 42 | 21 | 20.0 | 19 | 1 | hunan immun |
| 41 | 21 | 20.0 | 17 | 1 | hunan immun |
| 40 | 21 | 20.0 | 17 | 1 | hunan immun |
| 39 | 21 | 20.0 | 17 | 1 | hunan immun |
| 38 | 21 | 20.0 | 15 | 1 | hunan immun |
| 37 | 21 | 20.0 | 13 | 1 | hunan immun |
| 36 | 21.5 | 20.5 | 19 | 1 | hunan immun |
| 35 | 22 | 21.0 | 27 | 1 | hunan immun |
| 34 | 22 | 21.0 | 28 | 1 | hunan immun |
| 33 | 22 | 21.0 | 28 | 1 | hunan immun |
| 32 | 22 | 21.0 | 27 | 1 | hunan immun |
| 31 | 22 | 21.0 | 27 | 1 | hunan immun |
| 30 | 22 | 21.0 | 27 | 1 | hunan immun |
| 29 | 22 | 21.0 | 27 | 1 | hunan immun |
| 28 | 22 | 21.0 | 27 | 1 | hunan immun |
| 27 | 22 | 21.0 | 27 | 1 | hunan immun |
| 26 | 22 | 21.0 | 27 | 1 | hunan immun |
| 25 | 22 | 21.0 | 27 | 1 | hunan immun |
| 24 | 22 | 21.0 | 27 | 1 | hunan immun |
| 23 | 22 | 21.0 | 27 | 1 | hunan immun |
| 22 | 22 | 21.0 | 27 | 1 | hunan immun |
| 21 | 22 | 21.0 | 27 | 1 | hunan immun |
| 20 | 22 | 21.0 | 27 | 1 | hunan immun |
| 19 | 22 | 21.0 | 27 | 1 | hunan immun |
| 18 | 22 | 21.0 | 27 | 1 | hunan immun |
| 17 | 22 | 21.0 | 27 | 1 | hunan immun |
| 16 | 22 | 21.0 | 27 | 1 | hunan immun |
| 15 | 22 | 21.0 | 27 | 1 | hunan immun |
| 14 | 22 | 21.0 | 27 | 1 | hunan immun |
| 13 | 22 | 21.0 | 27 | 1 | hunan immun |
| 12 | 22 | 21.0 | 27 | 1 | hunan immun |
| 11 | 22 | 21.0 | 27 | 1 | hunan immun |
| 10 | 22 | 21.0 | 27 | 1 | hunan immun |
| 9 | 22 | 21.0 | 27 | 1 | hunan immun |
| 8 | 22 | 21.0 | 27 | 1 | hunan immun |
| 7 | 22 | 21.0 | 27 | 1 | hunan immun |
| 6 | 22 | 21.0 | 27 | 1 | hunan immun |
| 5 | 22 | 21.0 | 27 | 1 | hunan immun |
| 4 | 22 | 21.0 | 27 | 1 | hunan immun |
| 3 | 22 | 21.0 | 27 | 1 | hunan immun |
| 2 | 22 | 21.0 | 27 | 1 | hunan immun |
| 1 | 22 | 21.0 | 27 | 1 | hunan immun |

ALIGNMENTS

| | |
|--------|---|
| RESULT | 1 |
| ID | CXGT_CONTU |
| AC | P176d4; |
| DT | 01-AUG-1990 (Rel. 15, Created) |
| DT | 01-AUG-1990 (Rel. 15, Last sequence update) |
| DT | 01-NOV-1997 (Rel. 35, Last annotation update) |
| DE | CONANTOKIN-T (CON-T). |
| OS | Conus tulipa (fish-hunting cone snail) (Tulip cone). |
| OC | Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda; |
| OC | Neogastropoda; Conoidea; Conidae; Conus. |
| OX | NCBI_TaxId=6495; |
| RN | [1] |
| RP | SEQUENCE. |
| RC | TTSUP-Venom: |
| RX | MEDLINE=90202866; PubMed=2180939; |
| RA | Hack J.A., Rivier J.E., Parks T.N., Mena E.E., Cruz L.J., |
| RA | Oliviera B.M.; |
| RT | "conantokin-T. A gamma-carboxyglutamate containing peptide with |
| RT | N-methyl-D-aspartate antagonist activity."; |
| RL | J. Biol. Chem. 265:6025-6029(1990). |
| RN | [2] |
| RP | STRUCTURE BY NMR. |
| RX | MEDLINE=97388301; PubMed=9247135; |
| RA | Weider S.E., Chen Z., Zhu Y., Proxok M., Castellino F.J., Ni F.; |
| RT | "The NMR solution structure of the NMDA receptor antagonist, |
| RT | conantokin-T, in the absence of divalent metal ions."; |
| RL | FEBS Lett. 411:19-26(1997). |
| RN | [3] |
| RP | STRUCTURE BY NMR. |
| RX | MEDLINE=9753002; PubMed=899936; |
| RA | Sjkaebæk N., Nielsen K.J., Lewis R.J., Alewood P., Craik D.J.; |
| RT | "Determination of the solution structures of conantokin-G and |
| RT | conantokin-T by CD and NMR spectroscopy."; |
| RL | J. Biol. Chem. 272:2291-2299(1997). |
| CC | -I- FUNCTION: INDICES SLEEP-LIKE SYMPTOMS IN YOUNG MICE. INHIBITS |
| CC | N-METHYL-D-ASPARTATE (NMDA) RECEPTOR-MEDIATED CALCIUM INFLOW IN |
| CC | CENTRAL NERVOUS SYSTEM NEURONS. |
| DR | PIR: A35225; A35225. |
| DR | PDB: 1ONT; 04-SEP-97. |
| KW | Venom; Vitamin K; Gamma-carboxyglutamic acid; Calcium; Amidation; |
| KW | 3D-structure. |
| FT | MOD_RES 3 3 GAMMA-CARBOXYGLUTAMIC ACID. |
| FT | MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID. |
| FT | MOD_RES 10 10 GAMMA-CARBOXYGLUTAMIC ACID. |
| FT | MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID. |
| FT | MOD_RES 21 21 AMIDATION. |
| SQ | SEQUENCE 21 AA; 2509 MW; 7F7B893AC4d42C38 CRC64; |

| | | | | |
|-----------------------|--------|--------------------|-------|---------------|
| Query Match | 29.5% | Score 31; | DB 1; | Length 21; |
| Best Local Similarity | 41.2%; | Pred. No. 1.4e+02; | | |
| Matches | 7; | Conservative | 4; | Mismatches 6; |
| | | | | Indels 0; |
| | | | | Gaps 0 |
| QY | 4 | ELFENLERLDALOKK | 20 | |
| | ::: | :: | :: | |

DB 3 EEYOKMLENLEAEVKK 19

RESULT 2

ID END2_ONCKE STANDARD; PRT; 30 AA.

AC P01205;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE BETA-ENDOPHILIN II.

OS Oncorhynchus keta (Chum salmon).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

CC Proteocephali; Proteocephali; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_Taxid=8018;

RN [1]

RP SEQUENCE.

RX MEDLINE=80174902; PubMed=7370035;

RA Kawachi H., Tsubokawa M., Kanazawa A., Kitagawa H.;

RT "Occurrence of two different endorphins in the salmon pituitary.";

DR Biochem. Biophys. Res. Commun. 92:1278-1286(1980).

PIR: A01469; OEONZK.

KW Acetylation; Endorphin.

FT PEPTIDE 1 5 MET-ENKEPHALIN.

FT MOD.RES 1 1 ACETYLATION.

SO SEQUENCE 30 AA; 3527 MW; 98F68D5EB383D210 CRC64;

QY 1 PVLEFENLRL 10

DB 15 PLTLEFKNVI 24

Query Match 29.5%; Score 31; DB 1; Length 30;

Best Local Similarity 50.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 3

ID N006_SOLTU STANDARD; PRT; 19 AA.

AC P80729;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE NADH-UBIQUINONE OXIDOREDUCTASE 11 KDA SUBUNIT (EC 1.6.5.3)

DE (EC 1.6.99.3) (COMPLEX I-11KD) (CI-11KD) (FRAGMENT).

OS Solanum tuberosum (Potato).

CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

CC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;

CC Solanales; Solanaceae; Solanum.

OX NCBI_Taxid=4113;

RN [1]

RP SEQUENCE.

RA STRAIN=CV. BINTJE; TISSUE=Tuber;

RA Herz U., Grohmann L.;

RL Submitted (DEC-1996) to the SWISS-PROT data bank.

CC -I- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.

CC -I- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

CC -I- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.

CC -I- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER MEMBRANE.

CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion.

KW NON_TER 19 19

FT SEQUENCE 19 AA; 2310 MW; 0DCACEF407D79F49 CRC64;

Query Match 27.6%; Score 29; DB 1; Length 19;

Best Local Similarity 35.7%; Pred. No. 2.4e+02;

Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 VLELFENLRL 15

DB 3 IMEFANLILRME 16

RESULT 4

ID TMEF_RANFE STANDARD; PRT; 13 AA.

AC P66920;

DT 30-MAY-2000 (Rel. 39, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TEMPORIN E.

OS Rana temporaria (European common frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_Taxid=8407;

RN [1]

RP SEQUENCE.

RX MEDLINE=97175050; PubMed=9022710;

RA Stimaco M., Mignogna G., Canofeni S., Mele R., Mangoni M.L.,

RA Baria D.;

RT "Temporins, antimicrobial peptides from the European red frog Rana temporaria.";

RT Eur. J. Biochem. 242:788-792(1996).

CC -I- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIA.

CC -I- SUBCELLULAR LOCATION: SECRETED.

CC -I- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.

CC Amphibian skin; Antibiotic; Amidation; Multigene family.

FT MOD.RES 13 13 AMIDATION.

SO SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

QY 2 VLELFENLRL 14

DB 1 VLPITIGNLNSLL 13

Query Match 26.7%; Score 28; DB 1; Length 13;

Best Local Similarity 53.8%; Pred. No. 2.2e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 5

ID DMS4_PHYSA STANDARD; PRT; 27 AA.

AC P80280;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE DERMASEPTIN 4 (DS IV).

OS Phyllomedusa sauvagii (Sauvage's leaf frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

CC Phyllomedusa.

OX NCBI_Taxid=8395;

RN [1]

RP SEQUENCE.

RX MEDLINE=94139686; PubMed=8306981;

RA Mor A., Nicolas P.;

RT "Isolation and structure of novel defensive peptides from frog skin.";

RL Eur. J. Biochem. 219:145-154(1994).

CC -I- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPHATIC STRUCTURE.

CC -I- SUBCELLULAR LOCATION: SECRETED.

CC -I- TISSUE SPECIFICITY: SKIN.

KW Antibiotic; Fungicide; Multigene family; Amphibian skin.

SO SEQUENCE 27 AA; 2779 MW; 43C94D2DC19721A8 CRC64;

RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson S., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Matthey L., McDonald L., Artach P., Bowman C.,
RA

RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.":

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC with EMBL and the Sanger Institute.
 RL Nature 390:580-586(1997).
 RL -----

CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

UN Hypothetical protein. 30 AA; 3688 MW; FF79F03D0ACCCE4 CRC64

| | | | | |
|-----------------------|--------|------------------|-------|------------|
| Query Match | 24.8%; | Score 26; | DB 1; | Length 30; |
| Best Local Similarity | 50.0%; | Pred. No. 1e+03; | | |
| Matches | 6; | Conservative | 2; | Mismatches |
| | | | 4; | Indels |
| | | | | Gaps |
| | | | | 0 |

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Db      19  QNLLIFLNKKIK 30
          : ||      | || : |

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| TEMP_RANTE | TEMP_RANTE | STANDARD; | PRT; | 10 AA |
|------------|------------------------------|-----------|------|-------|
| ID | TEMP_RANTE | | | |
| AC | P56923; | | | |
| PT | 30-MAY-2000 (bol 30 created) | | | |

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN K.
OS *Rana temporaria* (European common frog).
NC Rana temporaria

| OX | NCBI_TaxID=8407; | NAME | NCBI_TaxID=8407; | NAME |
|----|------------------|------------------|------------------|------|
| RN | [1] | NCBI_TaxID=8407; | NCBI_TaxID=8407; | NAME |
| RP | SEQUENCE. | NCBI_TaxID=8407; | NCBI_TaxID=8407; | NAME |

RA "Temporins, antimicrobial peptides from the European red frog *Rana*
RT *temporaria*, and their analogues: synthesis and biological activity" *FEBS*
RA *lett.* 217:200, 1988. PubMed=3022210.

```

-|- SUBCELLULAR LOCATION: SECRETED.
CCC
-|- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
BACTERIA.
CCC

```

CC FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD_RES 10
SO SEQUENCE 10 AA. 1123 MW. 390549aa3727272457 CPG64.
AMIDATION.

| | | | | |
|-----------------------|--------|--------------------|-------|------------|
| Query Match | 23.8%; | Score 25; | DB 1; | Length 10; |
| Best Local Similarity | 60.0%; | Pred. No. 4.3e+02; | | |
| Marches | 6; | Consonanting | 1; | Missed |

| | | | |
|----|---|----------|----|
| 2y | 5 | LFENILRL | 14 |
| | 1 | : | 11 |
| Db | 1 | LPPNLKSL | 10 |

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RESULT 9
NIFD_ANASL STANDARD: PRT: 23 AA.
AC P3177;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1)
DE NITROGENASE COMPONENT 1 (NITROGENASE) (FRAGMENT).
GN NIFD.
NC Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
NCBI_TaxID=29412;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=93144353; PubMed=8424961;
RA Murphy S.T., Jackman D.M., Mulligan M.E.;
RT "Cloning and nucleotide sequence of the gene for dinitrogenase
reductase (nifH) from the heterocyst-forming cyanobacterium Anabaena
sp. L31."
RT Biochim. Biophys. Acta 1171:337-340(1993).
CC -1- FUNCTION: THE KEY ENZYMOLOGICAL REACTIONS IN NITROGEN FIXATION ARE
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CC -1- CATALYTIC ACTIVITY: 8 REDUCED FERREDOXIN + 8 H(+) + N(2) + 16 ATP
= 8 OXIDIZED FERREDOXIN + 2 NH(3) + 16 ADP + 16 ORTHOPHOSPHATE.
CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
30-32 FE, 2 MO, AND INORGANIC SULFUR.
CC -1- SIMILARITY: BELONGS TO THE NIFD/NIFK/NIFE/NIFN FAMILY.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L04499; AAA22015.1; -
CC PIR: S28191; S28191.
CC InterPro: IPR000318; -
CC PROSITE: PS00090; NITROGENASE_1_2; PARTIAL.
CC PROSITE: PS00699; NITROGENASE_1_1; PARTIAL.
CC Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.
KW NON TER
FT 23
SQ SEQUENCE 23 AA: 2666 MW: 9F2C70302E167806 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 23;
Best Local Similarity 31.2%; Pred. No. 1e+03;
Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 7 ENLEERLLDALOKKIK 22
DB 7 KNLYDENKELIOEVLR 22

RESULT 10
CT21_LITCI STANDARD: PRT: 26 AA.
AC P81847; P81848; P81849; P81850;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CITROPIN 2.1.3 [CONTAINS: CITROPIN 2.1.2; CITROPIN 2.1.1; CITROPIN
2.1.1].
DE Litoria citropa (Australian blue mountains tree frog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE.

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RC TISSUE=Skin;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Mahnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue
mountains tree-frog Litoria citropa. Solution structure of the
antibacterial peptide citropin 1.1."
RL Eur. J. Biochem. 265:627-637(1999).
CC -1- TISSUE SPECIFICITY: DORSAL AND SUBVENTRAL SKIN GLANDS.
FT PEPTIDE 1 22 CITROPIN 2.1.1.
FT PEPTIDE 1 23 CITROPIN 2.1.1.
FT PEPTIDE 1 25 CITROPIN 2.1.2.
FT PEPTIDE 1 26 CITROPIN 2.1.3.
SQ SEQUENCE 26 AA: 2519 MW: 7490C28EB2E4899A CRC64;

Query Match 23.8%; Score 25; DB 1; Length 26;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 13 LLDALOKKIK 22
DB 14 LVDVLRKRLQ 23

RESULT 11
TEND_RANTE
ID TEND_RANTE STANDARD: PRT: 13 AA.
AC P56918;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN C.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Baria D.;
RT "Temporalin, antimicrobial peptides from the European red frog Rana
temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
BACTERIA.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GABGURIN/RUGOSIN
FAMILY.
KW Amphibian skin; Antibiotic; Amidation; Multigene family.
FT MOD RES 13 13 AMIDATION.
FT SEQUENCE 13 AA: 1363 MW: 2201403A65582448 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 13;
Best Local Similarity 46.2%; Pred. No. 7.8e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 VLLEFENLEERLL 14
DB 1 LPLILGNLNGILL 13

RESULT 12
TEND_RANTE
ID TEND_RANTE STANDARD: PRT: 13 AA.
AC P56919;
DT 30-MAY-2000 (Rel. 39, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TEMPORIN D.

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| | RESULT | SHEEP | STANDARD: | PRT: | AA. |
|-----|---------------------|-----------------------------------|-----------|------|-----|
| ID | SECRETIN | | | | |
| SEC | SHEEP | | | | |
| PC | PJ3199; | | | | 27 |
| OT | 01-JUL-1993 | (Rel. 26, Created) | | | |
| UT | 01-JUL-1993 | (Rel. 26, last sequence update) | | | |
| DT | 01-NOV-1995 | (Rel. 32, last annotation update) | | | |
| EN | SECRETIN. | | | | |
| N | SCF. | | | | |
| DS | Ovis aries (Sheep). | | | | |

| RESULT | 15 |
|----------|---|
| MAIL RAT | |
| ID | MAIL RAT |
| AC | p57113; |
| DT | 01-OCT-2000 (Rel. 40, Created) |
| DT | 01-OCT-2000 (Rel. 40, Last sequence update) |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) |
| DE | MALEIYLACETOACETATE ISOMERASE (EC 5.2.1.2) (MAIL) (GLUTATHIONE S-DE TRANSFERASE ZETA 1) (EC 2.5.1.18) (GSTZ1-1) (FRAGMENT). |
| GN | GSTZ1. |
| OS | Rattus norvegicus (Rat). |
| OC | Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus |
| OX | NCBI_TaxId:101116; |
| OX | (1) |
| RP | SEQUENCE, AND CHARACTERIZATION. |
| RC | STRAIN=FISCHER 344; TISSUE=Liver; |
| RC | MEDLINE=98198370; PubMed=9531472; |
| RC | Tong Z., Board P.G., Anders M.W.; |
| RA | "Glutathione transferase zeta catalyses the oxygenation of the |
| RT | carcinogen dichloroacetic acid to glyoxylic acid."; |
| RT | Biochem. J. 331:371-374(1998). |
| CC | -I- FUNCTION: PROBABLE BIFUNCTIONAL ENZYME SHOWING MINIMAL |
| CC | GLUTATHIONE-CONJUGATING ACTIVITY WITH ETHACRINIC ACID AND 7- |
| CC | CHLORO-4-NITROBENZ-2-OXA-1,3-DIAZOLE AND MALEIYLACETOACETATE |
| CC | ISOMERASE ACTIVITY. HAS ALSO LOW GLUTATHIONE PEROXIDASE ACTIVITY |
| CC | WITH T-BUTYL AND CUMENE HYDROPEROXIDES (BY SIMILARITY). IS ABLE TO |
| CC | CATALYZE THE GLUTATHIONE DEPENDENT OXYGENATION OF DICHLOROACETIC |
| CC | ACID TO GLYOXYLIC ACID. |
| CC | -I- CATALYTIC ACTIVITY: 4-MALEIYLACETOACETATE = 4-FUMARYLACETOACETATE |
| CC | -I- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-G. |
| CC | -I- COFACTOR: THE MAIL ACTIVITY REQUIRES GLUTATHIONE (BY SIMILARITY). |
| CC | -I- PATHWAY: CATABOLISM OF TYROSINE; FOURTH STEP, CATABOLISM OF |
| CC | PHENYLALANINE, FIFTH STEP. |
| CC | -I- SUBUNIT: HOMODIMER (BY SIMILARITY). |

CC -1- SUBCELLULAR LOCATION: CYTOSOLPLASMIC.
CC -1- PTM: THE N-TERMINUS IS BLOCKED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE GST SUPERFAMILY, ZETA FAMILY.
KW Isomerase; Transferase; Multifunctional enzyme;
KW Phenylalanine catabolism; Tyrosine catabolism.
FT NON_TER 1 28
FT NON_TER 1 28
SQ SEQUENCE 28 AA; 2943 MW; 1070608C44491C25 CRC64;

Query Match 22.9%; Score 24; DB 1; Length 28;
Best Local Similarity 38.5%; Pred. NO. 1.7e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 NLERLDALQKK 20
| | | | | : |
DB 10 NALDKTIQSTAGK 22

Search completed: November 20, 2001, 09:45:52
Job time: 161 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2001, 09:43:26 ; Search time 20.8 seconds
(without alignments)
139.938 Million cell updates/sec

Title: US-08-940-096-146
Perfect score: 105
Sequence: 1 PYLELEFENLLERLDALQKKLK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 11509

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP unclassified: *
13: SP vertebrate: *
14: SP virus: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 35 | 33.3 | 26 | 2 | 025285 |
| 2 | 34 | 32.4 | 30 | 2 | 0918X1 |
| 3 | 34 | 32.4 | 30 | 2 | 0918W9 |
| 4 | 33 | 31.4 | 20 | 9 | 038458 |
| 5 | 31.5 | 30.0 | 29 | 4 | 090KSO |
| 6 | 31 | 29.5 | 23 | 11 | 09JINO |
| 7 | 29 | 27.6 | 20 | 13 | 09PS63 |
| 8 | 29 | 27.6 | 27 | 13 | P82847 |
| 9 | 28 | 26.7 | 15 | 11 | 090U25 |
| 10 | 28 | 26.7 | 16 | 6 | 09TRR2 |
| 11 | 28 | 26.7 | 25 | 14 | 036582 |
| 12 | 28 | 26.7 | 25 | 14 | 036585 |
| 13 | 28 | 26.7 | 25 | 14 | 036588 |
| 14 | 28 | 26.7 | 25 | 14 | 036591 |
| 15 | 28 | 26.7 | 25 | 14 | 036594 |
| 16 | 28 | 26.7 | 25 | 14 | 036597 |
| 17 | 28 | 26.7 | 27 | 14 | 09W7S6 |
| 18 | 28 | 26.7 | 29 | 11 | P97599 |
| 19 | 28 | 26.7 | 29 | 14 | 092646 |

| | | | | | | |
|----|------|------|----|----|--------|--------------------|
| 20 | 28 | 26.7 | 29 | 14 | 092648 | 092648 hepatitis e |
| 21 | 28 | 26.7 | 30 | 14 | 09WLK3 | 09WLK3 hepatitis e |
| 22 | 27 | 25.7 | 13 | 13 | P82881 | P82881 rana clamit |
| 23 | 27 | 25.7 | 19 | 2 | 09R4T9 | 09R4T9 bacillus th |
| 24 | 27 | 25.7 | 22 | 8 | P92621 | P92621 crotalus vi |
| 25 | 27 | 25.7 | 24 | 13 | 09PR22 | 09PR22 amia calva |
| 26 | 27 | 25.7 | 29 | 6 | 09XS75 | 09XS75 sus scrofa |
| 27 | 27 | 25.7 | 30 | 11 | 09QV95 | 09QV95 cavia (guin |
| 28 | 26 | 24.8 | 12 | 2 | 053183 | 053183 rhodococcus |
| 29 | 26 | 24.8 | 16 | 4 | 09UCY4 | 09UCY4 homo sapien |
| 30 | 26 | 24.8 | 17 | 2 | 09R5X6 | 09R5X6 mycoplasma |
| 31 | 26 | 24.8 | 20 | 8 | 092Y74 | 092Y74 mirax sp. c |
| 32 | 26 | 24.8 | 23 | 13 | P82398 | P82398 litoria ran |
| 33 | 26 | 24.8 | 23 | 13 | P82400 | P82400 litoria ran |
| 34 | 26 | 24.8 | 24 | 1 | 09UW11 | 09UW11 methanosarc |
| 35 | 26 | 24.8 | 24 | 13 | P82838 | P82838 rana berlan |
| 36 | 26 | 24.8 | 26 | 6 | 09TR25 | 09TR25 bos taurus |
| 37 | 26 | 24.8 | 27 | 5 | 09Y182 | 09Y182 priapulid c |
| 38 | 26 | 24.8 | 29 | 5 | 025603 | 025603 onchocerca |
| 39 | 25.5 | 24.3 | 21 | 11 | 008923 | 008923 mus musculu |
| 40 | 25 | 23.8 | 23 | 6 | 09TR81 | 09TR81 sus scrofa |
| 41 | 25 | 23.8 | 24 | 4 | 09UNM2 | 09UNM2 homo sapien |
| 42 | 25 | 23.8 | 25 | 4 | 09UED3 | 09UED3 homo sapien |
| 43 | 25 | 23.8 | 26 | 2 | 09F625 | 09F625 staphylococ |
| 44 | 25 | 23.8 | 26 | 13 | P82069 | P82069 litoria gen |
| 45 | 25 | 23.8 | 28 | 3 | 09U799 | 09U799 schizosacch |

ALIGNMENTS

RESULT 1
ID 025285 PRELIMINARY: PRT: 26 AA.
AC 025285:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 3.2 KDA PROTEIN.
GN HP0560 OR JHP0507.
OS Helicobacter pylori (Campylobacter pylori), and
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria: Proteobacteria: epsilon subdivision: Helicobacter group:
OC Helicobacter.
OX NCBI_TaxID=210, 85963;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA McEnteny B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=J99;
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tammlino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).

DR EMBL: AE000570; AAD07633.1; -
 DR EMBL: AE001484; AAD06083.1; -
 DR TIGR: HP0507; -
 DR TIGR: HP0560; -
 KW Hypothetical protein.
 SQ SEQUENCE 26 AA; 3169 MW; 34FE239BE3139AA1 CRC64;

Query Match 33.3%; Score 35; DB 2; Length 26;
 Best Local Similarity 58.3%; Pred. No. 4e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 9 ERLDALOKLK 20
 ID 15 LLYRLDVLBOK 26

RESULT 2
 ID Q9L8X1 PRELIMINARY; PRT; 30 AA.

AC Q9L8X1:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 15, last annotation update)
 DE POLYKETIDE SYNTHASE MODULE 6 (FRAGMENT).
 OS Streptomyces venezuelae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=54571;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC15068;
 RX MEDLINE=20179700; PubMed=10713461;
 RA Xue Y., Wilson D., Sherman D.H.;
 RT "Genetic architecture of the polyketide synthases for methymycin and pikromycin series macroides.";
 RL Gene 245:203-211(2000).
 DR EMBL: AF193251; AAF61860.1; -
 FT NON_TER 30
 SQ SEQUENCE 30 AA; 3562 MW; 673D2569873325A3 CRC64;

Query Match 32.4%; Score 34; DB 2; Length 30;
 Best Local Similarity 58.3%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 11 ERLDALOKLK 22
 ID 6 EQLVDALRASLK 17

RESULT 3
 ID Q9L8W9 PRELIMINARY; PRT; 30 AA.
 AC Q9L8W9:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 15, last annotation update)
 DE POLYKETIDE SYNTHASE MODULE 6 (FRAGMENT).
 OS Streptomyces nardonensis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=67333;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19790;
 RX MEDLINE=20179700; PubMed=10713461;
 RA Xue Y., Wilson D., Sherman D.H.;
 RT "Genetic architecture of the polyketide synthases for methymycin and pikromycin series macroides.";
 RL Gene 245:203-211(2000).
 DR EMBL: AF193252; AAF61862.1; -
 FT NON_TER 30

SQ SEQUENCE 30 AA; 3562 MW; 673D2569873325A3 CRC64;

Query Match 32.4%; Score 34; DB 2; Length 30;
 Best Local Similarity 58.3%; Pred. No. 6.3e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 11 ERLDALOKLK 22
 ID 6 EQLVDALRASLK 17

RESULT 4
 ID Q38458 PRELIMINARY; PRT; 20 AA.
 AC Q38458:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Bacteriophage phi-105.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 OX NCBI_TaxID=10717;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86056972; PubMed=3934047;
 RA Cully D.F., Garro A.J.;
 RT "Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophage phi 105: identification of the repressor gene and its RT mRNA and protein products.";
 RL Gene 38:153-164(1985).
 DR EMBL: M11920; AAA88402.1; -
 KW Hypothetical protein.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2342 MW; FCE3D10864EB54AA CRC64;

Query Match 31.4%; Score 33; DB 9; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.7e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 6 FENLERLDALOK 19
 ID 6 FEOLMAETKEALOK 19

RESULT 5
 ID Q9UKS0 PRELIMINARY; PRT; 29 AA.
 AC Q9UKS0:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)
 DE NUP98-RAP1GDS1 FUSION PROTEIN TYPE 2 (FRAGMENT).
 GN NRG2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hussey D.J., Nicola M., Moore S., Dobrovic A.;
 RT "The (4;11)(q21;p15) translocation fuses the NUP98 and RAP1GDS1 genes and is recurrent in T cell acute lymphocytic leukemia.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF133333; AAD54077.1; -
 FT NON_TER 1
 SQ SEQUENCE 29 AA; 2970 MW; A68E5D45DDCB205F CRC64;

Query Match 30.0%; Score 31.5; DB 4; Length 29;

RESULT 8

| ID | 36591 | PRELIMINARY; | PRT; | 25 AA. |
|----|--|--------------|----------|-------------------------|
| AC | 036591 | | | |
| DT | 01-JAN-1998 (TREMBLrel. 05, Created) | | | |
| DT | 01-JAN-1998 (TREMBLrel. 05, Last sequence update) | | | |
| DT | 01-JUN-2000 (TREMBLrel. 14, Last annotation update) | | | |
| DE | ORF-1 (FRAGMENT). | | | |
| OS | Hepatitis E virus. | | | |
| OC | Viruses; sarsna positive-strand viruses, no DNA stage | | | |
| OX | NCBI_Taxid=12461; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=MOROCO/FE23; | | | |
| RA | Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emme | | | |
| RA | Purcell R.; | | | |
| RL | J. Med. Virol. 0:0-0(1997). | | | |
| DR | EMBL:AF010420; AAB6538.1; -. | | | |
| FT | NON-TER | | | |
| SQ | SEQUENCE | 25 AA; | 2772 MW; | 5BVD6ECO36BHF038 CRC64; |

Query Match 26.7%; Score 28; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 3.2e+03;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PVLLEFENLIERL 13
 |||:|::|:|
 Db 12 PVLDTNLSILCRV 24

RESULT 15
 036594
 AC 036594; PRELIMINARY; PRT; 25 AA.
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE ORF-1 (FRAGMENT).
 OS Hepatitis E virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage.
 OX NCBI_TaxID=12461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUNISIA;
 RA Chatterjee R., Tsarev S., Pilot J., Coursaget P., Emerson S.,
 RA Purcell R.;
 RL J. Med. Virol. 0:0-0(1997).
 DR EMBL; AF010421; AAB66541.1; -.
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 2786 MW; B7AD6EC036BFF020 CRC64;

Query Match 26.7%; Score 28; DB 14; Length 25;
 Best Local Similarity 46.2%; Pred. No. 3.2e+03;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 1 PVLLEFENLIERL 13
 |||:|::|:|
 Db 12 PVLDTNLSILCRV 24

Search completed: November 20, 2001, 09:46:20
 Job time: 174 sec

